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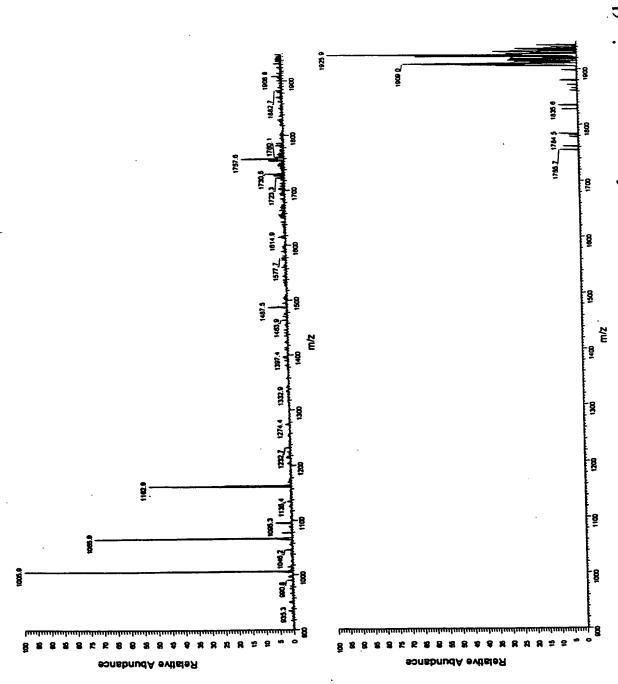


Figure 2. MS/MS of control RNA/DNA (upper); control+paromomycin (lower)

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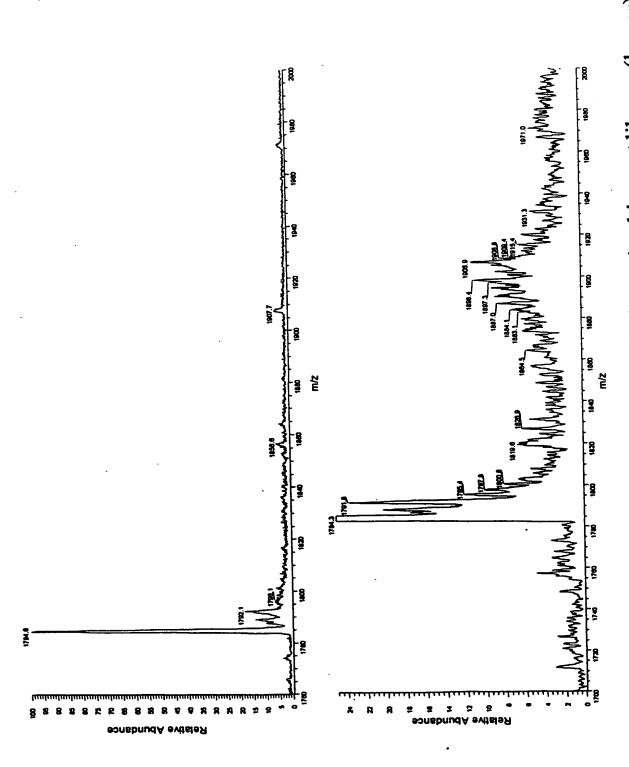


Figure 3. RNA/DNA chimera+paramomycin (upper); chimera+library (lower)

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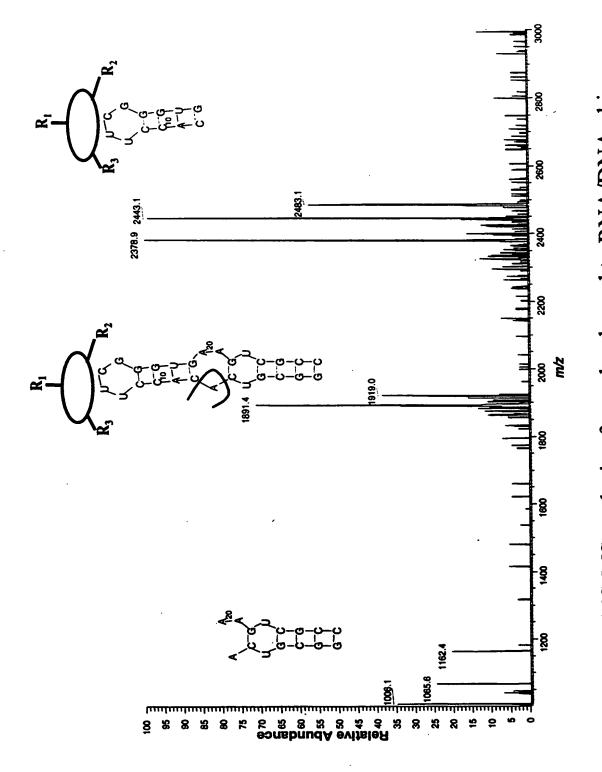
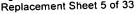


Figure 4. MS-MS analysis of member bound to RNA/DNA chimera

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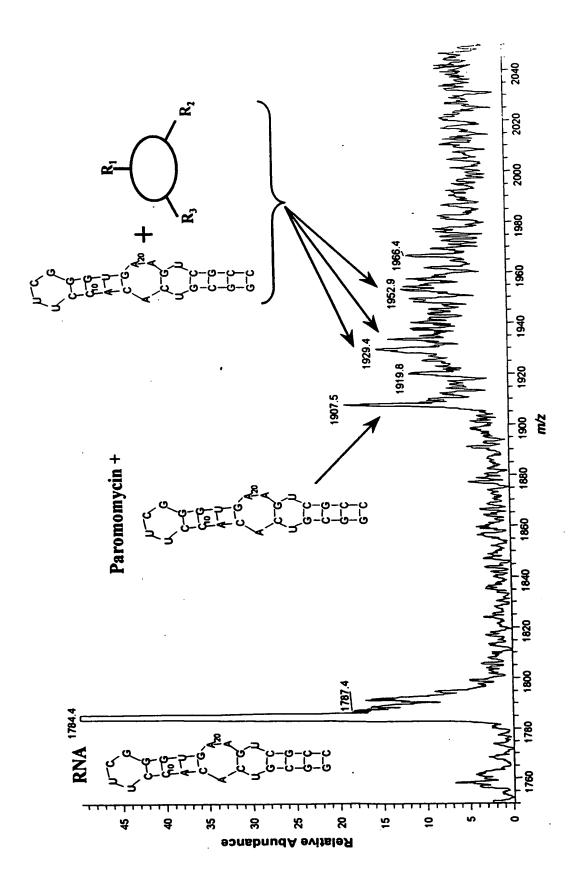


Figure 5. ESI-MS of RNA/DNA chimera bound to paromomycin and library

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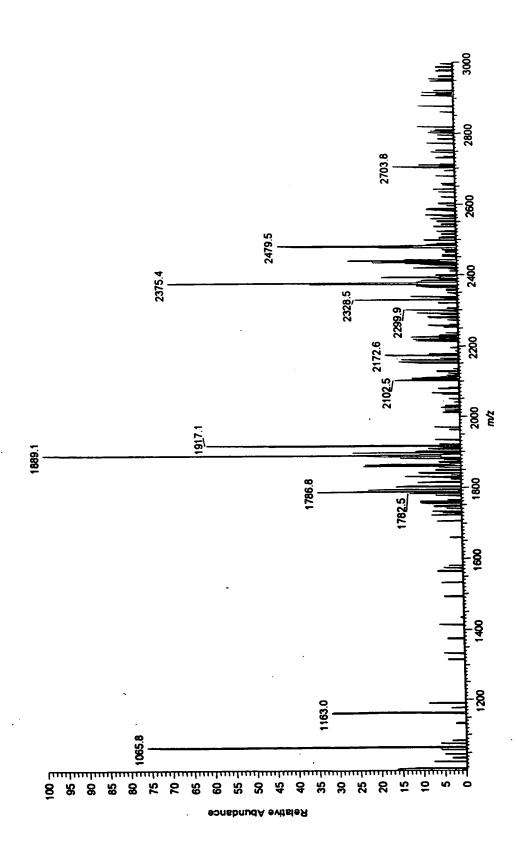


Figure 6. MS/MS of RNA/DNA chimera + compound with mass 665.1 not bound at the A-site

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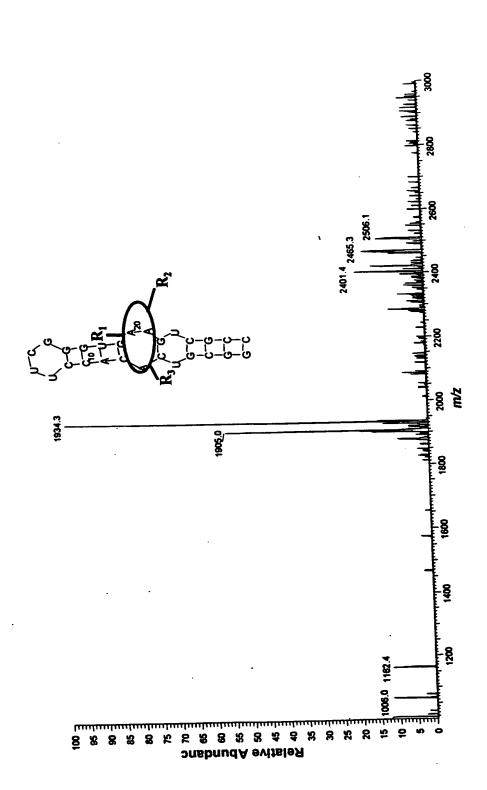


Figure 7. MS-MS analysis of member bound to RNA/DNA chimera at the A-Site

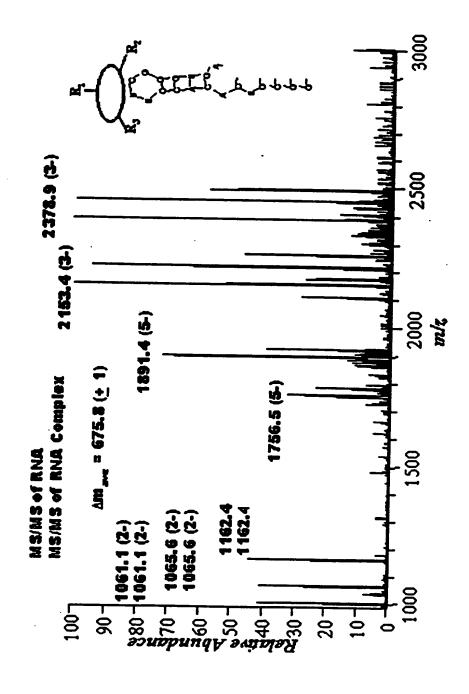
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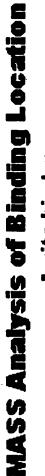
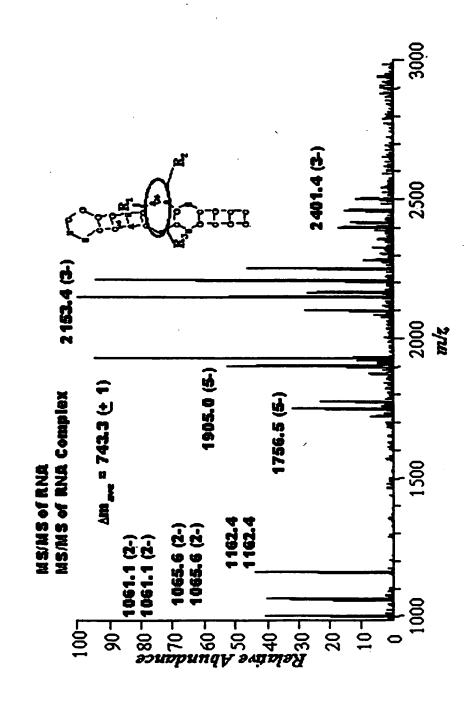
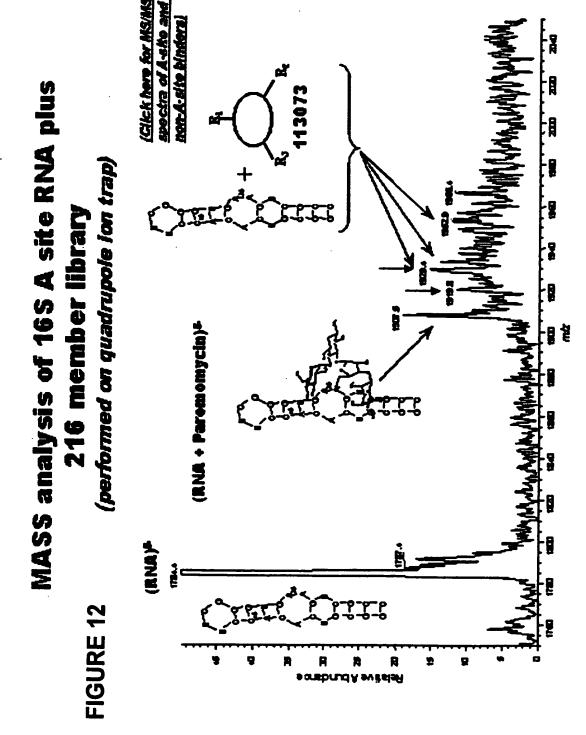




FIGURE 11



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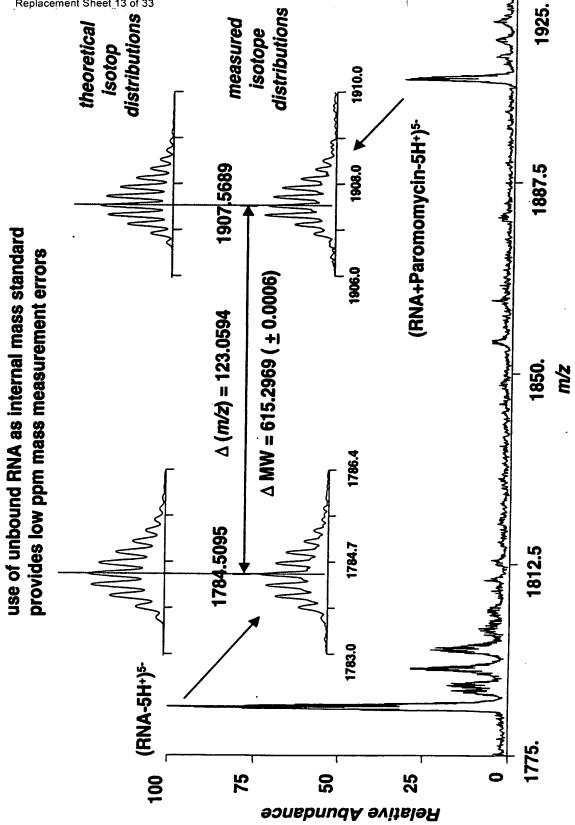


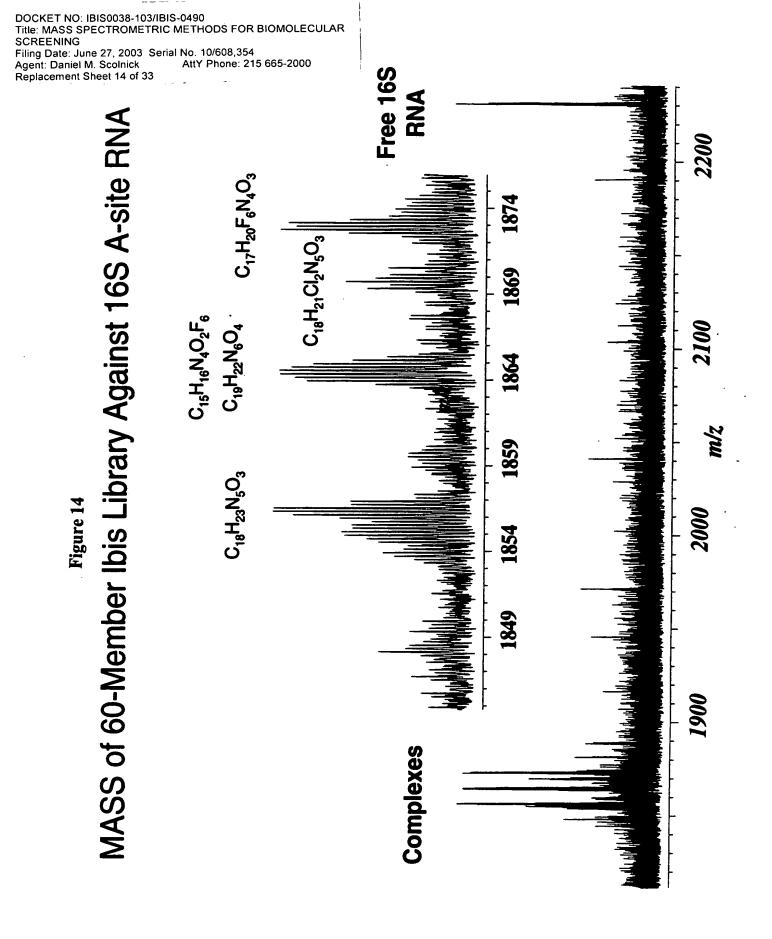
High Precision ESI-FTICR Mass Measurement of

Figure 13

16S A site RNA/Paromomycin Complex

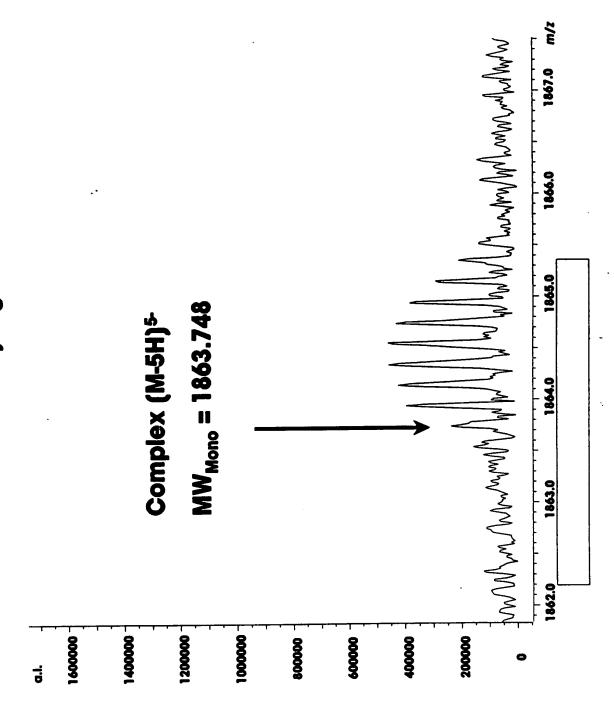
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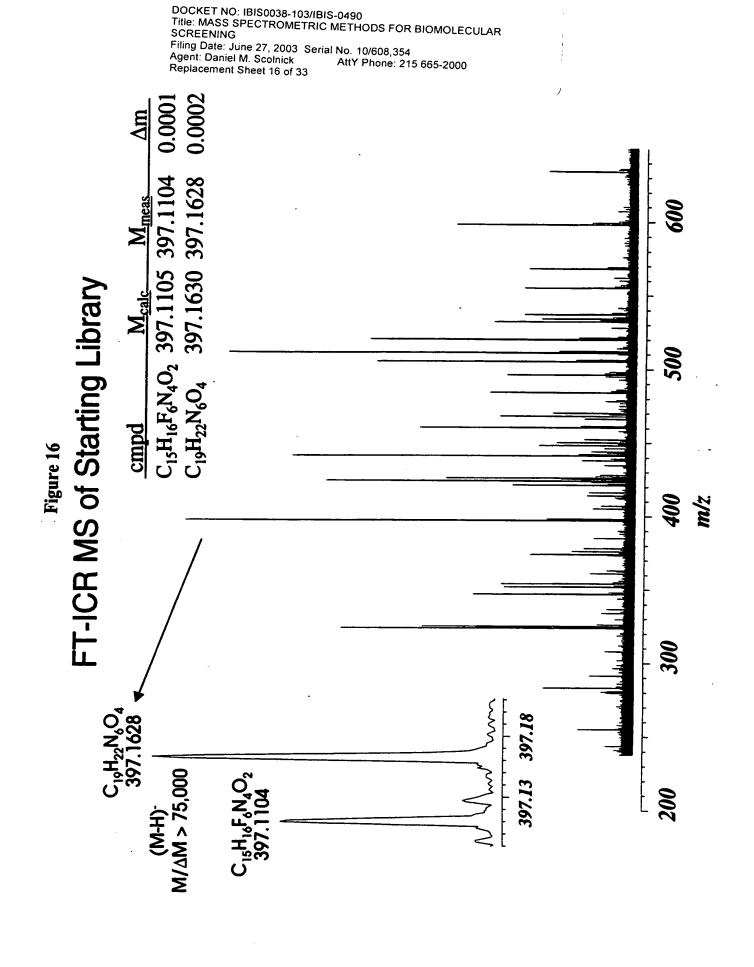




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MASS of 60-member Library against 16S A-site Model Figure 15





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Compound Identification from a 60-member Combinatorial library with MASS Figure 17

9320.300±.009 Da	8922.189±.009	398.111±.009 Da
Complex M _{meas}	RNA M _{meas}	ΔM

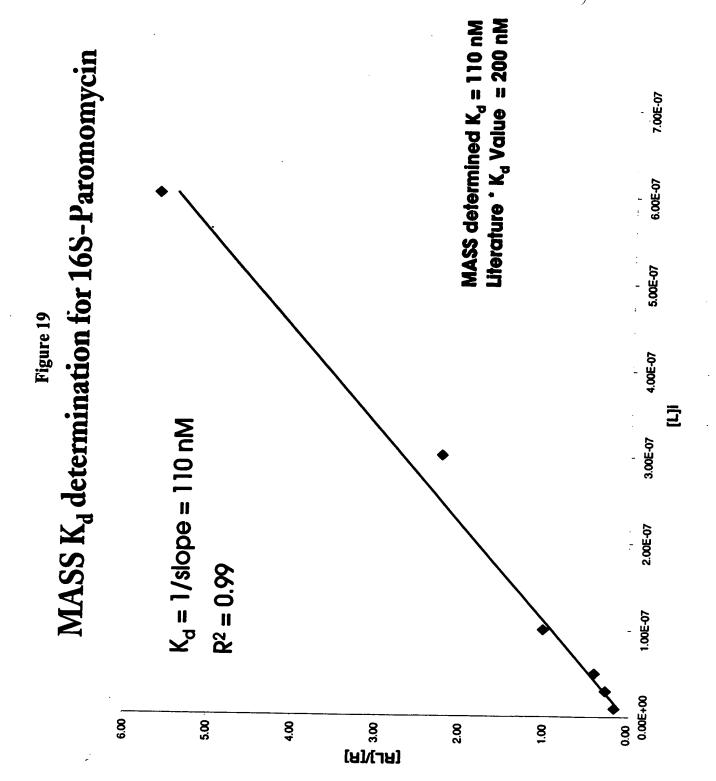
398.117 Da 998-163 $C_{15}H_{16}N_4O_2F_6$ -C19H2N6O4-

unintended products...

"Scaffold" C ₁₂ H ₂₃ N ₃ O ₇	Replaceme	NH2 NH2	of 33	-		Further constrain by	elemental composition of	"letters"
straints	\$ B	Ims OHO	OH HO	FE O O O O O O O O O O O O O O O O O O O	Ĭ		160, 14N ₁₉ 12C ₂₁ 1H ₃₃ 160, 14N ₁₃ 12C ₃ 1H ₃₃	16O ₁₄ 14N ₅ 12C ₂₃ 1H ₄₅
position Con	615.2969 1.0 ppm	toms Max. atoms	30 90 8	20 20	tal Compositions Error	(mdd)	96.0	0.97
emental Composition Constraints	Measured Mass: 615.2969 Mass Tolerance: 1.0 ppm Charge: 0	Element Min. atoms	¹² C 12 ¹ H 23	160 7 14N 3	Possible Elemental Compositions: Calc. Mass Error	(amu)	615.296291 615.296298	615.296305

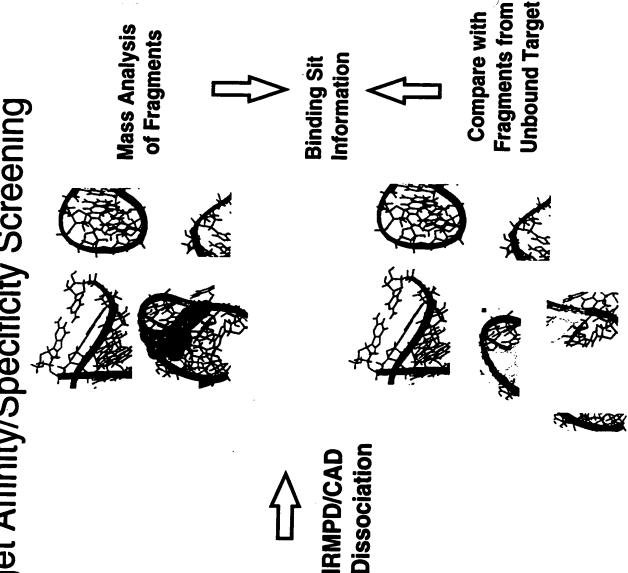
Figure 18

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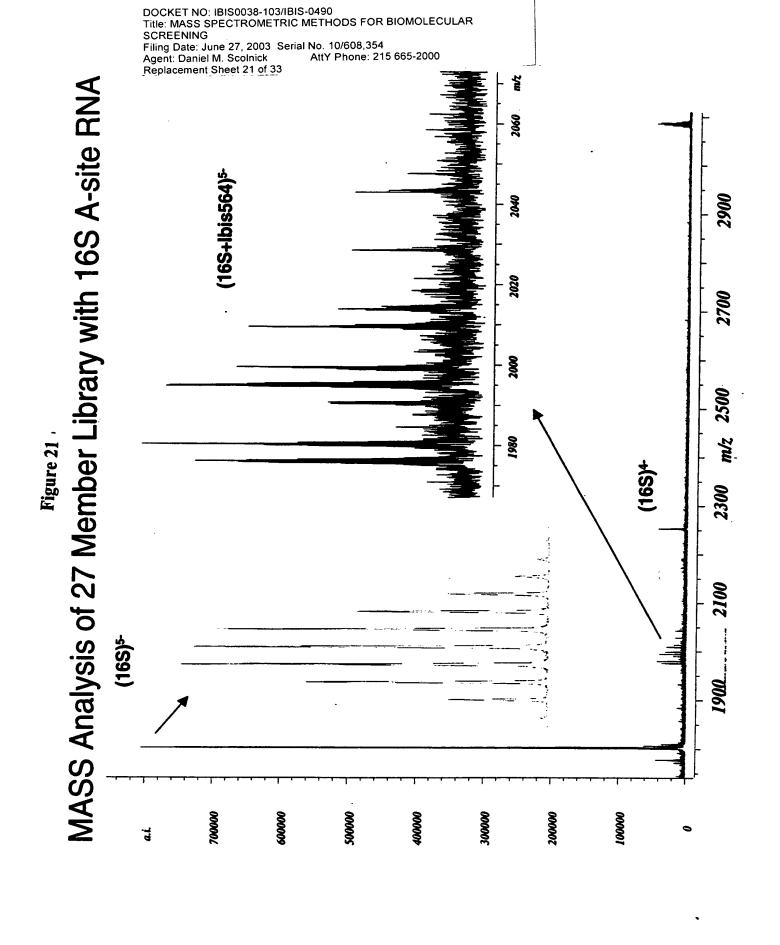


Mass Analysis of

Complex(es)

Intact

Multitarget Affinity/Specificity Screening Figure 20



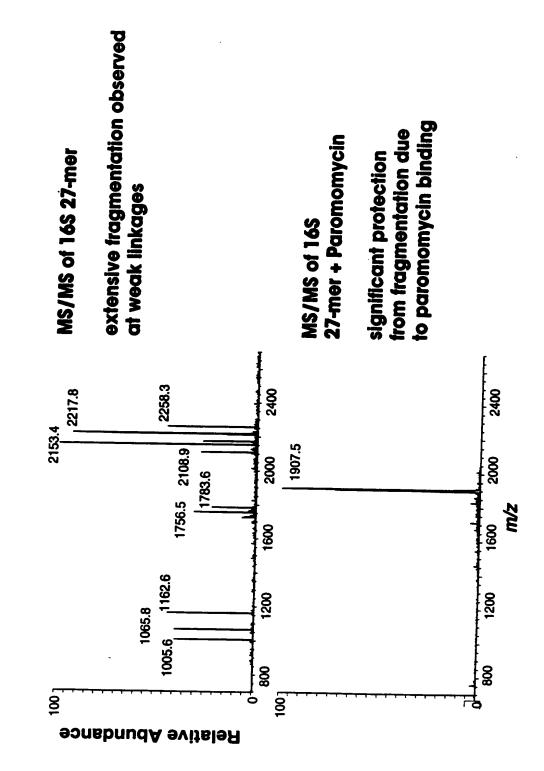
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MASS Protection Assay

Figure 22

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Atty Phone: 215 665-2000 Replacement Sheet 23 of 33 Reduced Fragmentation - Binding at A-site No protection - Binding not at A-site 1.8082 2483.1 2465.3 P.1045 2378.9 1934.3 88 0.3061 1.168 F 8

8

8

Relative Abundance

1162.4

1162.4

MASS Protection Assay

\$

Figure 23

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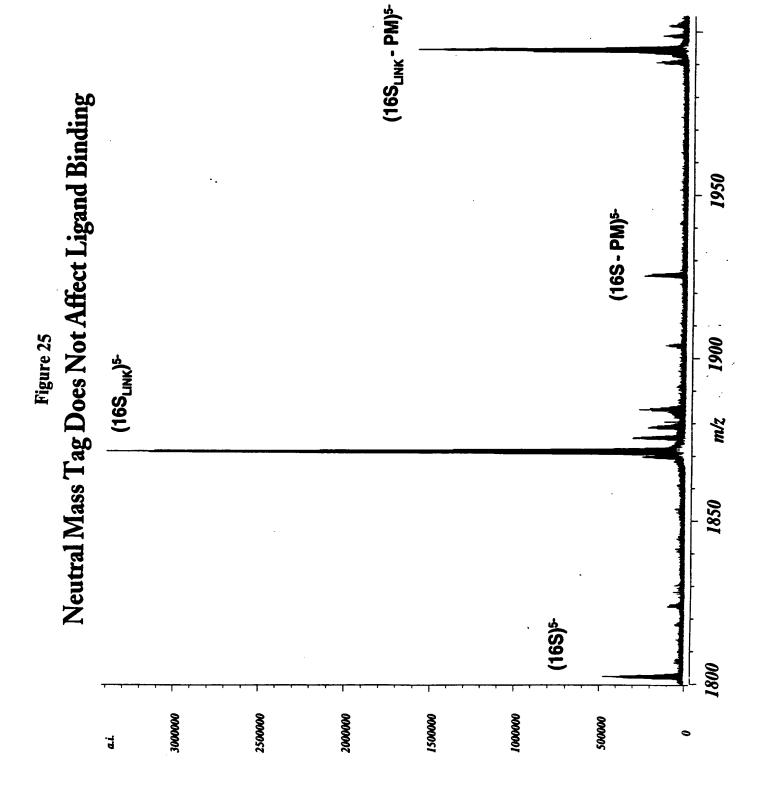
Figure 24

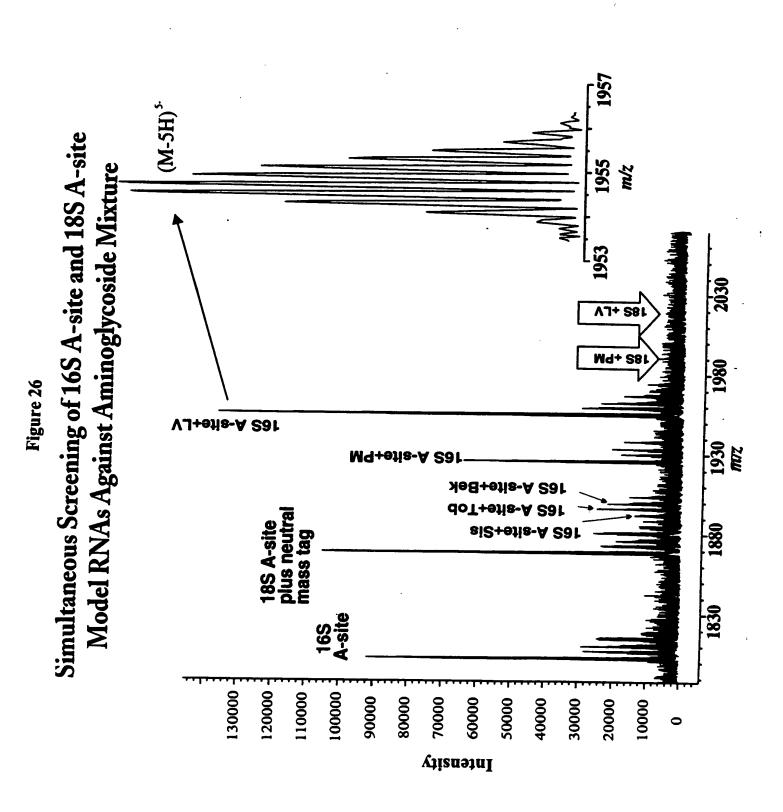
Eukaryotic and Prokaryotic A-Sit s

Aminoglycoside antibiotics bind to A-site of decoding region in 16S RNA

△ MW = 15.011 Da

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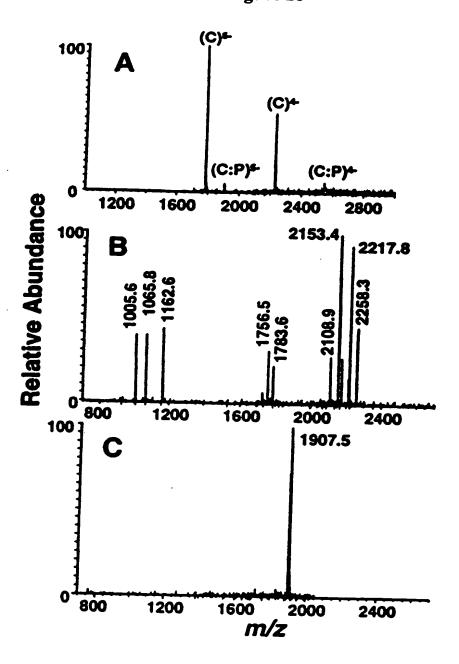
Figure 27

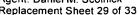
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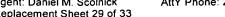
Figure 28

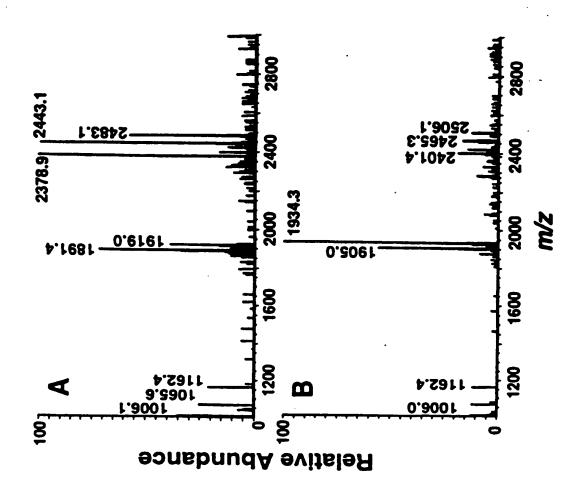




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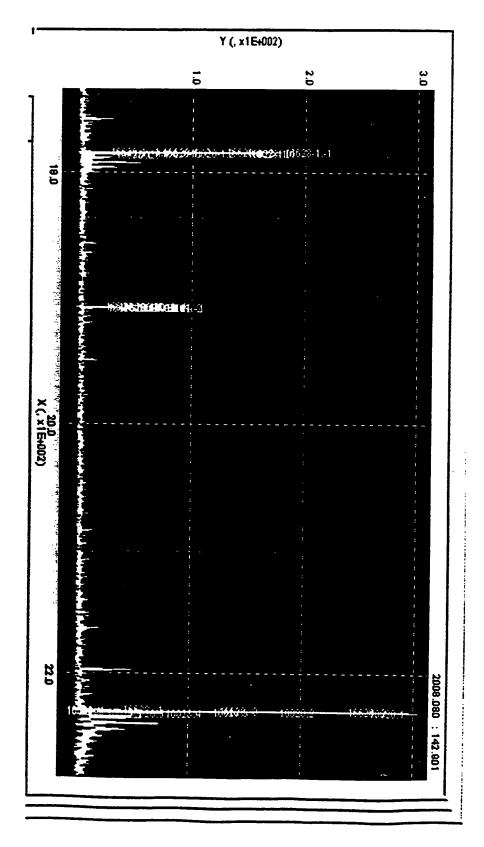
Figure 29





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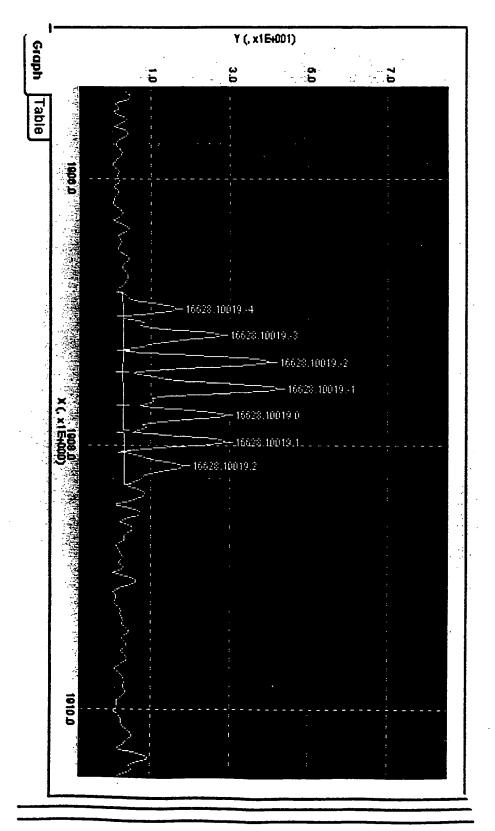


Figure 31

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	41.95	287.24	2231.023	2230.770	2230.887	16628.0	22
	40.90	280.66	2230.770	2230.516	2230.633	166281	21
	32.39	225.18	2230.516	2230.263	2230.380	20 166282	20
	16.23	111.72	2230.263	2230.029	2230.146	19 166283	19
	4.87	27.51	2230.029	2229.679	2229.874	166284	18
•	0.90	10.97	1908.271	1908.086	1908.157	16628.10019.2	17
	1.55	21.03	1908.043	1907.900	1907.972	16628.10019.1	16
	1.55	20.93	1907.843	1907.701	1907.772	16628.10019.0	15
	3.30	34.87	1907.701	1907.458	1907.572	16628.100191	14
	2.91	33.86	1907.444	1907.287	1907.373	3 16628.100192	13
	2.11	22.54	1907.273	1907.045	1907.173	16628.100193	12
	1.00	12.63	1907.031	1906.874	1906.974	16628.100194	11
	1.12	17.67	1785.569	1785.456	1785.506	16628-1.5	10
	2.65	32.31	1785.369	1785.232	1785.306	16628-1.4	9
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	8.56	82.63	1784.982	1784.795	1784.907	16628-1.2	7
	13.38	136.60	1784.795	1784.620	1784.707	16628-1.1	6
	14.74	133.94	1784.620	1784.433	1784.508	16628-1.0	5
	15.89	167.34	1784.383	1784.233	1784.308	16628-11	4
	11.14	115.60	1784.184	1784.021	1784.109	16628-12	3
	5.15	60.04	1783.972	1783.834	1783.909	16628-13	2
	1.63		.834	1783.635	1783.710	16628-14	1
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Figure 33

